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1	15	16	30	31	45	46	60	61	75	76	90
1 mtblder	MNELVDTTENYLRTI	YOLEEEGVTPLRARI	AERLDQSGPTVSQTV	SMERDGLLRVAGDR	HLELTEKGRALAIIV	MRKHRLAERLLVDVI					90
2 dtxr	MKDLVDTTENYLRTI	YELEEEGVTPLRARI	AERLEQSGPTVSQTV	ARMERDGLVVASD-	SLQHTPTGRTLATV	MRKHRLAERLLTDII					89
3 staphelislr	-----	---MTVSCPPPS--T	SEREQ-----	ARAL	CLRLLTARSRTRAEL	AGQLAKRGYPEDIGN	RVLDRLAAVGLVDDT				65
1	105	106	120	121	135	136	150	151	165	166	180
1 mtblder	GLPWEVHACACRWE	HVMSDEVERRLVKVL	NNPTTSPFGNPIPLG	VELGVGPPEGADDAN	LVRITELPAGSPVAV	VVRQLTEHVQGGDIDL					180
2 dtxr	GLIDINKVHDCACRWE	HVMSDEVERRLVKVK	DVSR-SPFGNPIPLG	DELGVGNS--DAAAP	GTRVIDAATSMERKV	RIVQJNEIFQVETDQ					176
3 staphelislr	DFAEQNVQSRANAA	KSKRALAAELHAKGV	DDDVITTVLGGIDAG	AERGRAEK--LVRAR	LRREVLIDOGTDEAR	VSRRLVAMHLARRG-Y					152
1	195	196	210	211	225	226	240	241	255	256	270
1 mtblder	ITRLKDAGVVPNARV	TVETTPGGGVITVIP	GHEVNTLPIEMHNAV	KVEKV	230						
2 dtxr	FQLLOADIRVGSEVE	IVORD--GHITLSHN	GKD-VELLDLIAHTI	RIEEL	223						
3 staphelislr	GOTLACEVVIIEALAA	ERERR--RV-----	-----	-----	174						

## FIGURE 1

## FIGURE 2

**SUBSTITUTE SHEET (RULE 26)**

09667-3103

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	10	20	30	40	50	60	
B1 DtxR		MKDLVDTTEM	YLRTIYELEE	EGIVPLRARI	AERLEQSGPT	VSQTVARMER	DGLVHVSPDR
Cd DtxR		MKDLVDTTEM	YLRTIYELEE	EGVTPLRARI	AERLEQSGPT	VSQTVARMER	DGLVVVASDR
Mt IdeR		MNELVDTTEM	YLRTIYDLEE	EGVTPLRARI	AERLDQSGPT	VSQTVSRMER	DGLLRVAGDR
Ms IdeR		MNDLVDTTEM	YLRTIYDLEE	EGVVPRLARI	AERLDQSGPT	VSQTVSRMER	DGLLRVAGDR
Ml IdeR		MNDLVDTTEM	YLRTIYDLEE	EGIVTPLRARI	AER	PT	VSQTVSRMER
Sl DesR		MSGLIDTTEM	YLRTILELEE	EGVVPRLARI	AERLDQSGPT	VSQTVARMER	DGLVSVAAADR
Se SirR	M	LTEEKED	YLKAILTNDG	DVSFVSNKKL	SQFLNIKPPS	VSEMVRLEK	EGYVETKHYK
Sa SirR	M	LTEEKED	YLKAILTNNG	DKNFVTNKIL	SQFLNIKPPS	VSEMVRLEK	AGYVETKPYK
Ef	M	TPNRED	YKLIFELGG	DEVKVNKKQI	VSGLDVSAAS	VSEMISKLVK	EDLVEHSPYQ
Sg	M	TPNKED	YLKCLYELGT	RHNKITNKEI	AGLMQVSPPA	VTEMMKKLLA	EELLIKDKKA
Sm	M	TPNKED	YLKIIYELSE	RDEKISNKQI	AEKMSVSAPA	VSEMVKKLLL	EDLVVKDKQA
Spn	M	TPNKED	YLKCIYEIGI	DLHKITNKEI	AARMQVSPPA	VTEMIKRMKS	ENLILKOEC
Spy	M	TPNKED	YLKCIYEIGI	DLHKITNKEI	AARMQVSPPA	VTEMIKRMKS	ENLILKDKEC
CONSENSUS		M--*-----E*	YL*-I*-----	-----NK-*	*-----P-	*****	*-L-----
		70	80	90	100	110	120
B1 DtxR		SLEMTPEGRS	LAIAMVRNDR	LAERLLTDII	GLDIHKVHDE	ACRWEHVMSD	EVERRLVEVL
Cd DtxR		SLQMTPTGRT	LATAVMRKHR	LAERLLTDII	GLDINKVHDE	ACRWEHVMSD	EVERRLVKVL
Mt IdeR		HLELTEKGRA	LAIAMVRKHR	LAERLLVDVI	GLPWEEVHAE	ACRWEHVMSD	DVERRLVKVL
Ms IdeR		HLELTDKGRA	LAVAMVRKHR	LAERLLVDVI	LPWEDGVHAE	ACRWEHVMSD	EVERRLVQVL
Ml IdeR		HLELTTKGRA	MAIAMVRKHR	LAERLLVDVI	GLPWEEVHAE	ACRWEHVMSD	DVERRLIKVL
Sl DesR		HLELTDGRR	LATRVMRKHR	LAERLLVDVI	GLEWEQVHAE	ACRWEHVMSD	AVERRVLELL
Se SirR		GARLTEEGLK	QTLDIKRRH	LLRLFLIEIL	QYNWEEVHQE	AEILEHRISD	LFVERLDKIL
Sa SirR		GVRLTEDGLT	HTLDII RHR	LLELFLIEIL	KYNWEEVHQE	AEILEHRISD	LFVERLDSLL
Ef		GVQLTEKGLK	KASTLIRKHR	IWEVFLVEHL	NYTWNDVHEE	AEVLEHVTSD	TLVNRADYL
Sg		GYLLTDLGLK	LVSDLYRKHR	LIEVFLVHHL	GYTTEEIHEE	AEVLEHTVSD	HFVERLDQLL
Sm		GYLLTKKGQI	LASSLYRKHR	LIEVFLMNHL	NYTADEIHEE	AEVLEHTVSD	VFVERLDKFL
Spn		GYLLTDLGLK	LVSELYRKHR	LIEVFLVHHL	DYTSDQIHEE	AEVLEHTVSD	LFVERLDKLL
Spy		GYLLTDLGLK	LVSELYRKHR	LIEVFLVHHL	DYTSDQIHEE	AEVLEHTVSD	LFVERLDKLL
CONSENSUS		---LT-G--	-----**HR	L--*L---L	-----H-E	A--*EH-S*	---*R---L
		130	140	150	160	170	180
B1 DtxR		DDVHRSPFGN	PIPLGLGEIGL	DQADEPDSGV	RAIDLPLGEN	LKARIVQVNE	ILQVDLEQFQ
Cd DtxR		KDVSRSPFGN	PIPLGLDELGV	GNSDAAAPGT	RVIDAATSMP	RKVRIVQVNE	IFQVETDQFT
Mt IdeR		NNPTTSPFGN	PIPLGLVELGV	GPEPGADDAN	LVRITELPAG	SPVAVVVRQL	TEHVQGDIDL
Ms IdeR		NNPTTSPFGN	PIPLGLTELAV	TPGVNTEDVS	LVRITELPVG	MPVAVVVRQL	TEHVQGDIDL
Ml IdeR		NNPTTSPFGN	PIPLGLDLGA	GPDAASANAK	LVRITELPVG	SPVAVVVRQL	TEHV DDIDL
Sl DesR		RHPTESPYGN	PIPLGLEELGE	TDGADPFLDE	GMVSLADLDP	GOEGKTVVVR	RIGEPIDTDA
Se SirR		NFPKTCPHGG	VIP	R GNSDAAAPGT	SILNFEPGER	VTVRRV RRDK	TELL
Sa SirR		NFPKTCPHGG	VIP	R NNEYKEYIT	TILNYEPGDI	VTIKRV RDK	TDLL
Ef		NHPEFCPHGG	VIPEDNQPIH	EEKROTLDY	PVGTKIRIAR	VLDEKELLDY	LVSIDLNIQE
Sg		DYPKACPHGG	TIPAKGELLV	EKHKLTLEEA	KEKGDYILAR	VHDNFDLLTY	LERNGLQVQK
Sm		NYPKVCPHGG	TIPGHGOPLV	ERYRTTLKGV	TEMGVYLLKR	VQDNFOLLKY	MEQHHLKIGD
Spn		GFPKTCPHGG	TIPAKGELLV	EINNPLADI	KEAGAYRLTR	VHDSFDILHY	LDKHSILHIGD
Spy		GFPKTCPHGG	TIPAKGELLV	EINNPLADI	KEAGAYRLTR	VHDSFDILHY	LDKHSILHIGD
CONSENSUS		--P--*P*G*	-IP-----*	-----	-----	-----	-----

FIGURE 3

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	190	200	210	220	230
B1 DtxR	ALTDAGVEIG	TEVDIINEQG	RVVITHNGSS	VELIDDLAHA	VRVEKVEG
Cd DtxR	QLLDADIRVG	SEVEIVDRDG	HITLSHNGKD	VELLDDLAHT	IRIEEL
Mt IdeR	ITRLKDAGVV	PNARVTVETT	PGGGVTVIVIP	GHENVTLPHE	MAHAVKVEKV
Ms IdeR	IGRLKEAGVV	PNARVTVEAN	NNGGVMIVIP	GHEQVELPHH	MAHAVKKKVE KVEKV
Ml IdeR	ITRLKDTGVV	PNARVTVETS	PAGNVIIIIP	GHENVTLPHE	MAHAVKVEKV

S1 DesR	QLMYTLRRAG	VQPGSVVSVT	ESAGGVLVGS	GGEAAELEAD	TASHVFVAKR
Sa SirR	VYLSSKDIYI	GNTVEIVSKD	DTNKVIILKR	NDIVTILSYE	NAMNIFAEK
Sa SirR	IYLSSKDISI	GNEVEIVSKD	EMNKVIIIKR	NDNVIIIVSYE	NAMNMFAEK
Ef	EYTIKEIAAY	EGPITIYNEN	KELSVSFKAA	NTIFVEPLIR	ESEEN
Sg SgoR	TIRFLGYDDF	SHLYSLEVDG	QEIQLAQPIA	QQIYVEKI	
Sm SloR	ELRLLEYDAF	AGAYTIEKDG	EQLQVTSAVA	SQIYIEKKAY	
Spn	QLQVKQFDGF	SNTFTILSND	EDLQVNMDIA	KQLYVEKIN	
Spy	QLQVKQFDGF	SNTFTILSND	EDLQVNMDIA	KQLYVEKIN	

CONSENSUS -----

FIGURE 3 cont.

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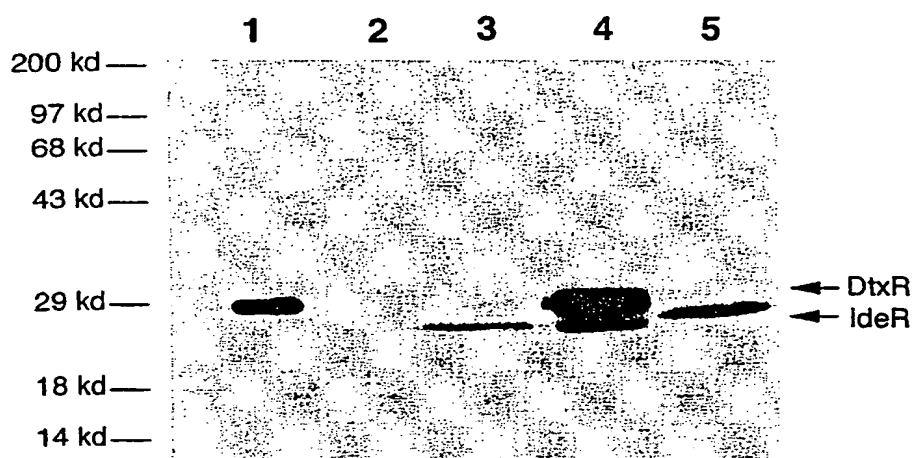


FIGURE 4

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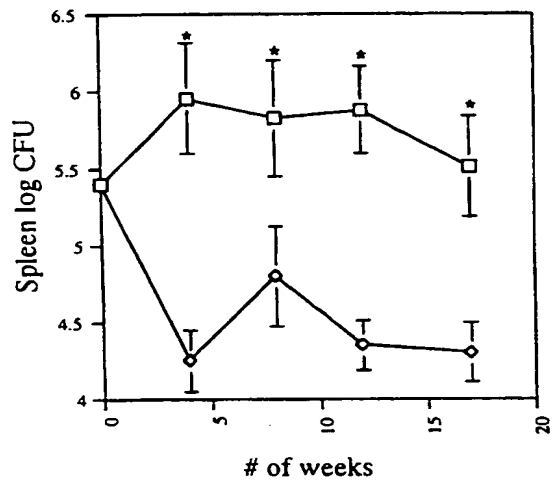


FIGURE 5A

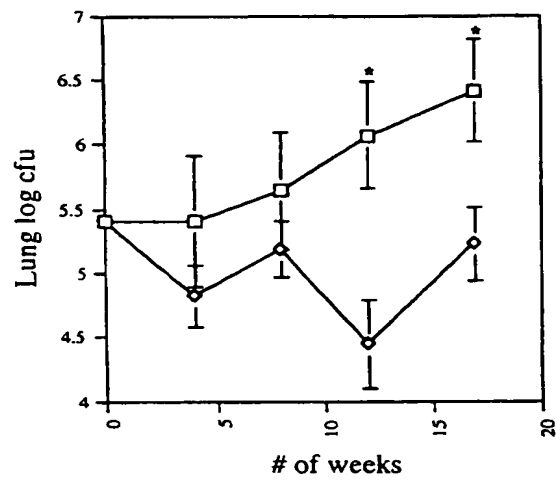


FIGURE 5B

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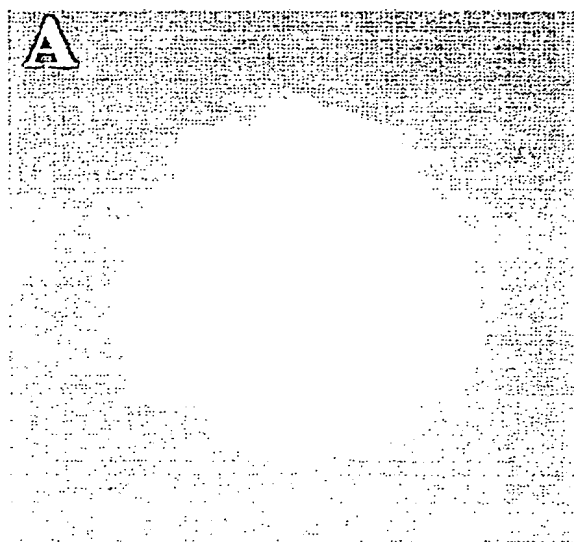


FIGURE 6A

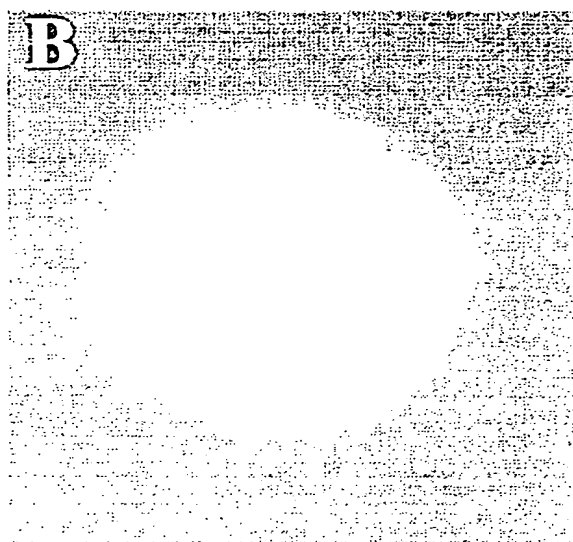


FIGURE 6B



G	T	A	G	G	T	T	A	G	G	C	T	-	A	A	C	C	T	A	T	Consensus Sequence
T	T	A	G	G	T	T	A	G	G	C	T	-	A	A	C	C	T	A	A	Published Consensus
T	T	A	G	G	A	T	A	G	C	T	T	-	T	A	C	C	T	A	A	<i>tox</i> PO <i>C.diphtheriae</i>
T	T	A	G	G	T	T	A	G	G	C	T	-	C	A	C	C	T	A	A	<i>desA</i> PO <i>S.pilosus</i>
C	C	A	G	G	G	T	A	T	C	T	A	-	A	T	C	C	T	G	T	16S ribosomal RNA
G	C	A	G	G	C	C	A	G	T	G	A	-	A	A	C	C	T	G	T	19 kDa antigen
A	C	A	G	G	T	G	G	T	G	C	T	C	A	A	C	C	A	C	G	<i>htrA</i> homologue
G	A	A	G	G	T	A	A	C	G	T	T	C	A	A	C	C	A	A	T	<i>phoP</i> homologue
G	C	A	G	G	T	G	A	C	C	G	T	C	A	A	C	C	G	A	T	<i>adhB</i> homologue
G	A	A	G	G	T	C	A	A	C	C	A	-	A	A	C	A	A	G	A	<i>narG</i> homologue

FIGURE 7

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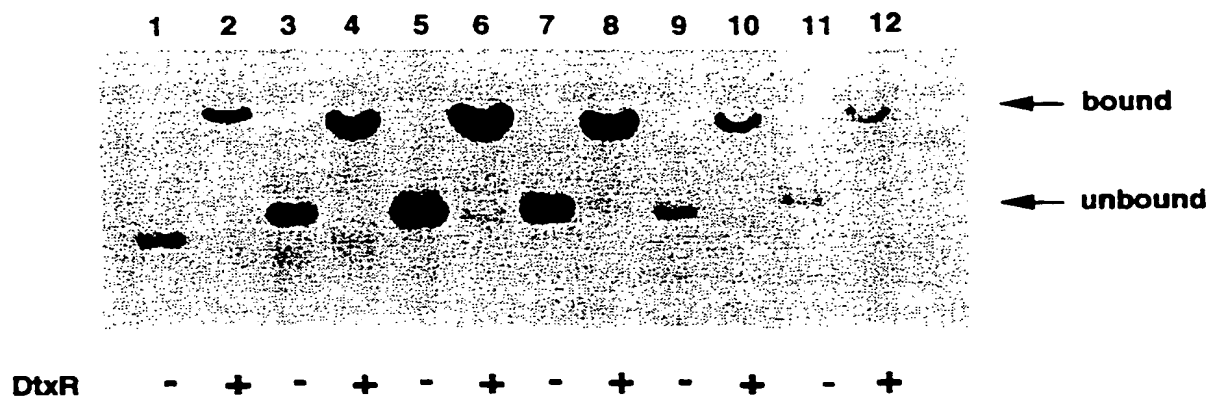


FIGURE 8

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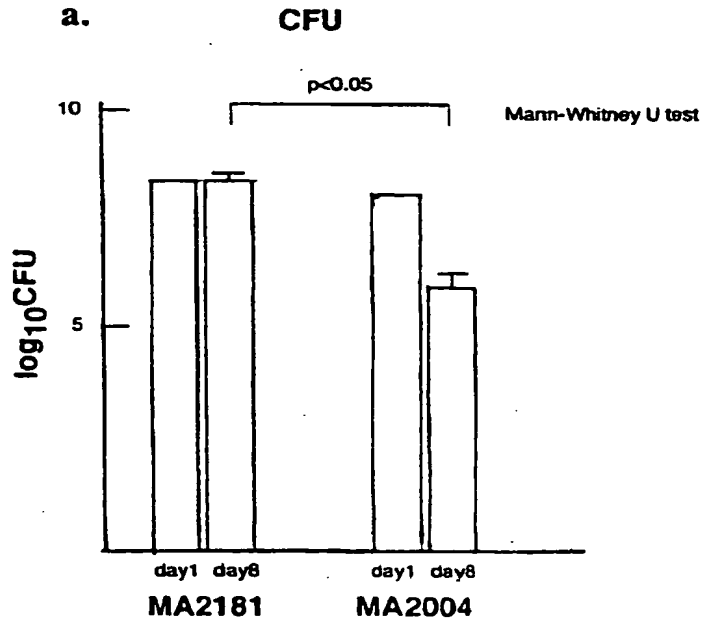


FIGURE 9A

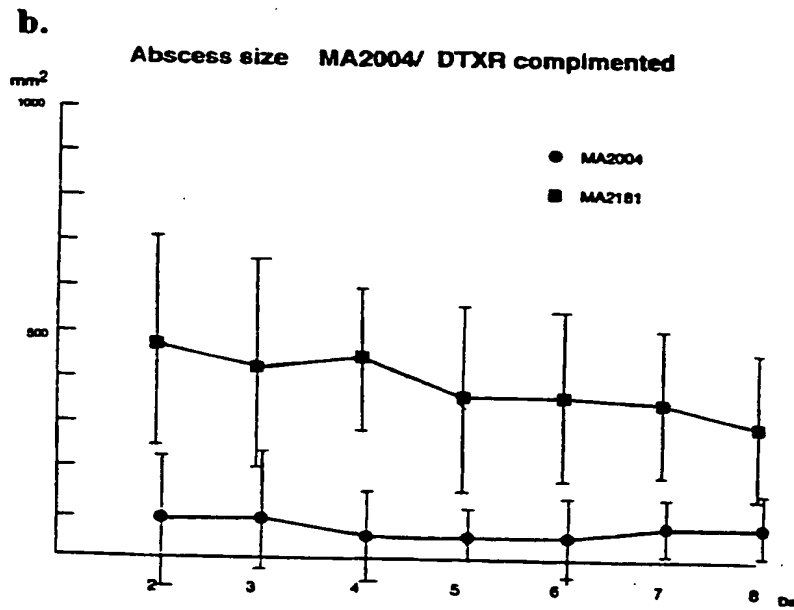


FIGURE 9B